

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 09/378,045D
Source: FFW/6
Date Processed by STIC: 5-3-05

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IFW16

RAW SEQUENCE LISTING

DATE: 05/03/2005

PATENT APPLICATION: US/09/378,045D

TIME: 13:26:38

Input Set : A:\2625-E REV.4.14.05.ST25.txt

Output Set: N:\CRF4\05032005\I378045D.raw

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3 <110> APPLICANT: Rauch, Charles
4   Walczak, Henning
6 <120> TITLE OF INVENTION: RECEPTOR THAT BINDS TRAIL
8 <130> FILE REFERENCE: 2625-E
10 <140> CURRENT APPLICATION NUMBER: US 09/378,045D
11 <141> CURRENT FILING DATE: 1999-08-20
13 <150> PRIOR APPLICATION NUMBER: US 08/883,036
14 <151> PRIOR FILING DATE: 1997-06-26
16 <150> PRIOR APPLICATION NUMBER: US 08/869,852
17 <151> PRIOR FILING DATE: 1997-06-04
19 <150> PRIOR APPLICATION NUMBER: US 08/829,536
20 <151> PRIOR FILING DATE: 1997-03-28
22 <150> PRIOR APPLICATION NUMBER: US 08/815,255
23 <151> PRIOR FILING DATE: 1997-03-12
25 <150> PRIOR APPLICATION NUMBER: US 08/799,861
26 <151> PRIOR FILING DATE: 1997-02-13
28 <160> NUMBER OF SEQ ID NOS: 6
30 <170> SOFTWARE: PatentIn version 3.2
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 1323
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
38 <220> FEATURE:
39 <221> NAME/KEY: CDS
40 <222> LOCATION: (1)..(1323)
42 <400> SEQUENCE: 1
43 atg gaa caa cgg gga cag aac gcc ccg gcc gct tcg ggg gcc cgg aaa      48
44 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
45 1          5          10          15
47 agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct ggg ccc      96
48 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
49          20          25          30
51 cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg ctg ttg      144
52 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
53          35          40          45
55 gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct ccc cag      192
56 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
57          50          55          60
59 cag aga gcg gcc cca caa caa aag agg tcc agc ccc tca gag gga ttg      240
60 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
61 65          70          75          80
63 tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc atc tcc      288
64 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser

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65	85	90	95	
67 tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc ctt ttc				336
68 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe				
69	100	105	110	
71 tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta agt ccg				384
72 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro				
73	115	120	125	
75 tgc acc acg acc aga aac aca gtg tgt cag tgc gaa gaa ggc acc ttc				432
76 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe				
77	130	135	140	
79 cgg gaa gaa gat tct cct gag atg tgc cgg aag tgc cgc aca ggg tgt				480
80 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys				
81 145	150	155	160	
83 ccc aga ggg atg gtc aag gtc ggt gat tgt aca ccc tgg agt gac atc				528
84 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile				
85	165	170	175	
87 gaa tgt gtc cac aaa gaa tca ggt aca aag cac agt ggg gaa gcc cca				576
88 Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro				
89	180	185	190	
91 gct gtg gag gag acg gtg acc tcc agc cca ggg act cct gcc tct ccc				624
92 Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro				
93	195	200	205	
95 tgt tct ctc tca ggc atc atc ata gga gtc aca gtt gca gcc gta gtc				672
96 Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val				
97	210	215	220	
99 ttg att gtg gct gtg ttt gtt tgc aag tct tta ctg tgg aag aaa gtc				720
100 Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val				
101 225	230	235	240	
103 ctt cct tac ctg aaa ggc atc tgc tca ggt ggt ggt ggg gac cct gag				768
104 Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu				
105	245	250	255	
107 cgt gtg gac aga agc tca caa cga cct ggg gct gag gac aat gtc ctc				816
108 Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu				
109	260	265	270	
111 aat gag atc gtg agt atc ttg cag ccc acc cag gtc cct gag cag gaa				864
112 Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu				
113	275	280	285	
115 atg gaa gtc cag gag cca gca gag cca aca ggt gtc aac atg ttg tcc				912
116 Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser				
117	290	295	300	
119 ccc ggg gag tca gag cat ctg ctg gaa ccg gca gaa gct gaa agg tct				960
120 Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala Glu Arg Ser				
121 305	310	315	320	
123 cag agg agg agg ctg ctg gtt cca gca aat gaa ggt gat ccc act gag				1008
124 Gln Arg Arg Arg Leu Val Pro Ala Asn Glu Gly Asp Pro Thr Glu				
125	325	330	335	
127 act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg ccc ttt gac				1056
128 Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp				
129	340	345	350	

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131 tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat gag ata      1104
132 Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile
133      355      360      365
135 aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg tac acg      1152
136 Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr
137      370      375      380
139 atg ctg ata aag tgg gtc aac aaa acc ggg cga gat gcc tct gtc cac      1200
140 Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His
141 385      390      395      400
143 acc ctg ctg gat gcc ttg gag acg ctg gga gag aga ctt gcc aag cag      1248
144 Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln
145      405      410      415
147 aag att gag gac cac ttg ttg agc tct gga aag ttc atg tat cta gaa      1296
148 Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu
149      420      425      430
151 ggt aat gca gac tct gcc atg tcc taa      1323
152 Gly Asn Ala Asp Ser Ala Met Ser
153      435      440
156 <210> SEQ ID NO: 2
157 <211> LENGTH: 440
158 <212> TYPE: PRT
159 <213> ORGANISM: Homo sapiens
161 <400> SEQUENCE: 2
163 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
164 1      5      10      15
167 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
168      20      25      30
171 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
172      35      40      45
175 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
176      50      55      60
179 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
180 65      70      75      80
183 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
184      85      90      95
187 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
188      100      105      110
191 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
192      115      120      125
195 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
196      130      135      140
199 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
200 145      150      155      160
203 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
204      165      170      175
207 Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro
208      180      185      190
211 Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro
212      195      200      205

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Output Set: N:\CRF4\05032005\I378045D.raw

```

215 Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
216      210      215      220
219 Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val
220 225      230      235      240
223 Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu
224      245      250      255
227 Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu
228      260      265      270
231 Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu
232      275      280      285
235 Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser
236      290      295      300
239 Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala Glu Arg Ser
240 305      310      315      320
243 Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp Pro Thr Glu
244      325      330      335
247 Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp
248      340      345      350
251 Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile
252      355      360      365
255 Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr
256      370      375      380
259 Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His
260 385      390      395      400
263 Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln
264      405      410      415
267 Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu
268      420      425      430
271 Gly Asn Ala Asp Ser Ala Met Ser
272      435      440
275 <210> SEQ ID NO: 3
276 <211> LENGTH: 157
277 <212> TYPE: DNA
278 <213> ORGANISM: Homo sapiens
281 <220> FEATURE:
282 <221> NAME/KEY: CDS
283 <222> LOCATION: (3)..(155)
285 <220> FEATURE:
286 <221> NAME/KEY: misc_feature
287 <222> LOCATION: (145)..(145)
288 <223> OTHER INFORMATION: n is a, c, g, or t
290 <220> FEATURE:
291 <221> NAME/KEY: misc_feature
292 <222> LOCATION: (149)..(149)
293 <223> OTHER INFORMATION: n is a, c, g, or t
295 <400> SEQUENCE: 3
296 ct gag act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg ccc
297      Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro
298      1      5      10      15

```

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Output Set: N:\CRF4\05032005\I378045D.raw

```

300 ttt gac tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat      95
301 Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn
302                20                25                30
304 gag ata aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg      143
305 Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
306                35                40                45
W--> 308 tnc acn atg ctg at      157
309 Xaa Thr Met Leu
310                50
313 <210> SEQ ID NO: 4
314 <211> LENGTH: 51
315 <212> TYPE: PRT
316 <213> ORGANISM: Homo sapiens
318 <220> FEATURE:
319 <221> NAME/KEY: misc_feature
320 <222> LOCATION: (48)..(48)
321 <223> OTHER INFORMATION: The 'Xaa' at location 48 stands for Tyr, Cys, Ser, or Phe.
323 <400> SEQUENCE: 4
325 Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe
326 1                5                10                15
329 Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu
330                20                25                30
W--> 333 Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Xaa
334                35                40                45
337 Thr Met Leu
338                50
341 <210> SEQ ID NO: 5
342 <211> LENGTH: 8
343 <212> TYPE: PRT
344 <213> ORGANISM: Artificial Sequence
346 <220> FEATURE:
347 <223> OTHER INFORMATION: FLAG peptide
349 <400> SEQUENCE: 5
351 Asp Tyr Lys Asp Asp Asp Asp Lys
352 1                5
355 <210> SEQ ID NO: 6
356 <211> LENGTH: 3159
357 <212> TYPE: DNA
358 <213> ORGANISM: Artificial Sequence
360 <220> FEATURE:
361 <223> OTHER INFORMATION: Cloning Vector pGP1k
363 <400> SEQUENCE: 6
364 aattagcggc cgctgtcgac aagcttcgaa ttcagtatcg atgtggggta cctactgtcc      60
366 cgggattgcg gatccgcgat gatatcggtg atcctcgagt gcggccgcag tatgcaaaaa      120
368 aaagcccgcg cattaggcgg gctcttggca gaacatatcc atcgcgtccg ccatctccag      180
370 cagccgcacg cggcgcatct cgggcagcgt tgggtcctgg ccacgggtgc gcatgatcgt      240
372 gtcctgtctg ttgaggaccc ggctaggctg gcgggggttg cttactgggt agcagaatga      300
374 atcaccgata cgcgagcgaa cgtgaagcga ctgctgctgc aaaacgtctg cgacctgagc      360
376 aacaacatga atggtcttcg gtttccgtgt ttcgtaaagt ctggaaacgc ggaagtcagc      420

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/03/2005
PATENT APPLICATION: US/09/378,045D TIME: 13:26:39

Input Set : A:\2625-E REV.4.14.05.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 145,149

Seq#:3; Xaa Pos. 48

Seq#:4; Xaa Pos. 48

VERIFICATION SUMMARY

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Input Set : A:\2625-E REV.4.14.05.ST25.txt

Output Set: N:\CRF4\05032005\I378045D.raw

L:308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:143

M:341 Repeated in SeqNo=3

L:333 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:32